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Listing first 45 summaries
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A; Title: Characterization of a human and murine gene (CLCN3) sharing A; Reference number: A57067; MUID:95394449; PMID:7665160
A; Accession: I48295
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-760 < RES>
A; Cross-references: EMBL:X78874; NID:9854275; PIDN:CAA55476.1; PID:98:0.; Genetics: A; Gene: Clcn3
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chloride channel 3 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #te
C; Accession: 148295; S55473
R; Borsani, G; Rugarli, E.I; Taglialatela, M.; Wong,
Genomics 27, 131-141, 1995
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Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999;
Accession: I48295; S55473
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A; Cross-references: GB:D17521;
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A:Title: Cloning and expression
A:Reference number: I58159; MUII
A:Accession: I58159
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C;Species: Rattus rattus (black rat, roof rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-
C;Accession: I58159
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                                                                                                                                          32 MTNGGSINSSTHLLDLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKESAWEM
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                                                                                                                                                                                                                                   ClC-3
                        TTFEERDKCPOWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFAPYACG
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                                                                                                    TKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCCWGSNE
                                                                                                                               MTNGGSINSSTHLLDLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKESAWEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKL
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                                                                                                                                                                                             Similarity
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                  translated from
                                                                                                                                                                                                                                                                                                                                                              S.; Monkawa, T.;
                                                                                                                                                                                            95.6%;
99.5%;
                                                                                                                                                                                                                                                                                                                          sion of a protein MUID:94206538; PM
                                                                                                                                                                                                                                                            NID: g473727; PIDN: BAA04471.1;
                                                                                                                                                                                Score 3994; DB 2;
Pred. No. 8.2e-306;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     roof rat)
on 26-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                  GB/EMBL/DDBJ
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chloride channel - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Accession: 137242
R.yan Slegtenhorst, M.A.; Bassi, M.T.; Borsani, G.; Wapenaar, M.C.; Ferrero, R.yan Slegtenhorst, M.A.; Bassi, M.T.; Borsani, G.; Wapenaar, M.C.; Ferrero, Hum. Mol. Genet. 3, 547-552, 1994
A.;Title: A gene from the Xp22.3 region shares homology with voltage-gated characteristics: 137242; MUID:94348498; PMID:8069296
A.;Accession: 137242; MUID:94348498; PMID:8069296
A.;Accession: 137242
A.;Status: preliminary; translated from GB/EMBL/DDBJ
A.;Molecule type: mRNA
A.;Residues: 1-760 <RES>
A.;Cross-references: EMBL:X77197; NID:g479158; PIDN:CAA54417.1; PID:g479159
A.;Cross-references: EMBL:X77197; NID:g479158; PIDN:CAA54417.1; PID:g479159
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A;Cross:reference
A;Map position: X
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Best Local
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Map position: Xp22.3-Xp22.3
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                                                                                                 GLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMEN 791
TTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFAPYACG
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                                         IKSLLDAWSGWVVMLLIGLLAGTLAGVIDLAVDWMTDLKEGVCLSAFWYSHEQCCWTSNE
                                                           TKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCCWGSNE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARKKQEGVVGSSRVCFAQHTPSLPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDVFRKL
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                GDB:270666; OMIM:302910
                                                                                                                                                                          78.4%;
77.9%;
                                                                                                                                                             83;
                                                                                                                                                           Score 3273; DB 2;
Pred. No. 4.1e-249;
3; Mismatches 85;
                                                                                                                                                                                     Length
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A; Molecule type: mRNA
A; Residues: 1-747 <SCH>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data
A; Reference number: S47327
A; Accession: S47327
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                              chloride channel protein 3 - rat
C;Species: Rattus norvegicus (Norway ra
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S47327
R;Schwappach, B.; Jentsch, T.J.
                                                                                                                                                                                                             Matches
   121
                                    165
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                                                                                    LDLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKESAWEMTKSLYDAWSGWLV
                TWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFAPYACGSGIPEIKTILSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 791
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                                                                    MLLIGLLAGTLAGVIDLAVDWMTDLKEGVCLSAFWYSHEQCCWTSNETTFEDRDKCPLWQ
                                                                                                                                         MDFLDEPFPDVGTYEDFHTIDWLREKSRDTDRHRKITSKSKESIWEFIKSLLDAWSGWVV
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                                                                                                                                                                                                           586;
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                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                            EMBL: Z36944; NID: g535931; PIDN: CAA85406.1;
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78.48;
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                                                                                                                                                                                                                          Score 3240; DB 2;
Pred. No. 1.6e-246;
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gene Clcn4 protein - mouse
C;SpecLes: Mus muscullus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1
C;Accession: I48294
R;Rugarli, E.I.; Adler, D.A.; Borsani, G.; Tsur
Nature Genet. 10, 466-471, 1995
A;Tille: Different chromosomal localization of
A;Reference number: I48294; MUID:95400329; PMII
A;Accession: I48294
A;Status: preliminary; translated from GB/EMBL,
A;Molecule type: mRNA
A;Residues: 1-747 <RES>
A;Cross-references: EMBL:Z49916; NID:9929679; I
C;GenetLcs:
A;Gene: Clcn4
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                                                                                                                                                    Local Similarity
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  TWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFAPYACGSGIPEIKTILSGF
                                         MLLIGLLAGTLAGVIDLAVDWMTDLKEGVCLSAFWYSHEQCCWTSNETTFEDRDKCPLWQ
                                                                  VTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEOCCWGSNETTFEERDKCPQWK 164
                                                                                                                             MDFLEEPFPDVGTYEDFHTIDWLREKSRDTDRHRKITSKSKESIWEFIKSLLDAWSGWVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCFAQHTPSLPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKLGLRQCLVTHNGRL
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                         EMBL: 249916; NID: g929679;
                                                                                                                                                                                                                                 77.0%;
77.6%;
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                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                 3217; DB 2;
No. 1e-244;
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PMID:7670496
                                                                                                                                                                                                                                                                                                                                         PIDN:CAA90150.1;
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T19065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable protein kinase C-regulated chloride channe C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C:Accession: T19065; T25256 R:Percy, C
                                                                                                                                               A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-735 <WI2>
                                                                                                                                                                                                             A; Reference number: A; Accession: T25256
                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: Z20005
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-735 <WIL>
A; Cross-references: EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19068
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                                       A; Map position:
                                                                A; Gene:
                                                                                                       A; Cross-references: EMBL: Z54216; A; Experimental source: clone T24+
                                                                                                                                                                                                                                                                         R; Lightning,
                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary;
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                                                             CESP:C07H4.2
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                      81/3;
                                                                                                                                                                                                                                                                                                                     EMBL: 268334;
                                                                                                                                                                                                                                                                                                 clone
                                                                                                                                                                                                                                                                                                                                                                                   translated
                      242/3;
                                                                                                                                                                                                                                                     Library,
                                                                                                                                                                                                                                                                                                 C07H4
                      297/3;
                                                                                                                           PIDN:CAA90949.1; GSPDB:GN00020; CESP:C07H4
                                                                                                                                                                                                                                                                                                                       PIDN:CAA92728.1;
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                                                                                                                                                                                                                                                       September
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                   337/2;
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537/3;

634/2;

GSPDB:GN00020;

CESP:C07H4

#text_change

Caenorhabditis 29-Oct-1999

elegans

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MYFTEEPPELPANSPHPLKLRRIFNLSPFTVTDHTPMETVVDIFRKLGLRQCLVTRSGRL
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                                                                                                                                                           AAAVTSKWVADAFGKEGIYEAHIHLNGYPFLDVKDEFTHRTLATDVMRPRREEPPLSVLT
                                                                                                                                                                           AAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTLAADVMRPRRNDPPLAVLT
                                                                                                                                                                                                                          HHDWIIFRNWCRPGADCVTPGLYAMVGAAACLGGVTRMTVSLVVIMFELTGGLEYIVPLM
                                                                                                                                                                                                                                           HHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSLVVIVFELTGGLEYIVPLM
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Gaps

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C;Accession: 137277

R;Fisher, S.E.; Black, G.C.; Lloyd, S.E.; Hatchwell, E.; Wrong Hum. Mol. Genet. 3, 2053-2059, 1994

A;Title: Isolation and partial characterization of a chloride A;Reference number: I37277; MUID:95179126; PMID:7874126

A;Accession: I37277

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I37277
                                                                                                                                                                                                                                                                                        RESULT
137277
    A;Cross-references: EMBL:X81836;
C;Genetics:
                                        A; Molecule type: mRNA
A; Residues: 1-260 < RES>
                                                                                                                                                                                                                                                              chloride channel protein, kidney -
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                     NID: 9577052;
                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                S.E.; Hatchwell, E.; Wrong,
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                     PIDN:CAA57430.1;
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                     PID:g577053
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A;Gene: CCP
A;Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-772 < PYL>
A;Cross-references: GB:AEO01274; NID:g3264850; PIDN:AAC24628.1;
A;Experimental source: strain MHOM/IL/81/Friedlin
A;Experimental source: strain MHOM/IL/81/Friedlin
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A;Cross-references: GDB:433706; C
A;Map position: Xp11.23-Xp11.22
A;Note: defects in this gene may
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Matches
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                                    IFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSFF
                                                                                                                                                                                      GSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFAP
                                                                                                                                                                                                                                           YGDKWSVYSPEGEAFFAAMACGIVLGCLGVFSDACAHWVSAFRSGICANFFWLGRNMCCV
                                                                                                                                                                                                                                                                                 Y-DAWS-----GWLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKKDI 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENMINETSYNGFPVIMSKESORLVGFALRRDLTIAIESARKKQEGIVGSSRVCFAQHTPS 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTLAADVMRPRRNDPPLAVLTQDNMTVDDI
                                                                              YASGGGIAEVKTIVSGHHVKRYLGGWTLITKVVGMCFSTGSGLTVGKEGPFVHIGACVGG
                                                                                                                  YACGSGIPEIKTILSGFIIRGYLGKWTLMIKTITLVLAVASGLSLGKEGPLVHVACCCGN
                                                                                                                                                                                                                                                                                                                         GADESITNLVVNVSEA-----DWATIDCIRSHTEAAE---RAAMWRRHSATAAASSS
                                                                                                                                                                                                                                                                                                                                                                  GSINSSTHLLDLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKESAWEMTKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETIISETTYSGFPVVVSRESQRLVGFVLRRDLIISIENARKKQDGVVSTSIIYFTEHSPP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADALGREGIYDAHIRLNGYPFLEAKEEFAHKTLAMDVMKPRRNDPLLTVLTQDSMTVEDV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPPYTPPTLKLRNILDLSPFTVTDLTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKKDV
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                            -----CGEYYSWGEFFLGRDNHVVAFV-DFVMYVSFSTMAAVTAAYLCKTYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.0%;
79.1%;
                                                                                                                                                                                                                                                                                                                                                                                                      24.4%; Score 1020.5; DB 32.0%; Pred. No. 5.5e-72; tive 140; Mismatches 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMIM: 300009
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Pred. No. 9.5e-78;
9; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nephrolithiasis 2, X-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39817
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-812 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SPBC19C7.11 - fission yeast (Schizosaccharomyces C; Species: Schizosaccharomyces pombe
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Matches
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                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                              64
GPGSYIMNYIMYIFWALSFAFLAVSLVKVFAPYACGSGIPEIKTILSGFIIRGYLGKWTL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGVTAVLLQSRVDLWHTGRIVQESVNYQHNWHEFELPMEAAIGCEGGEMGSTESVVNLHV
                                           MIKTITLVLAVASGLSLGKEGPLVHVACCCGNIFSYLFPKYSTNEAKKREVLSAASAAGV 295
                                                                                                                                                                                                      TDLKEGICLSALWYNHEQCCWGS------NETTFEERDKCPQWKTWAELIIGQAE 175
                                                                                                                                                                                                                                                                                    KDRERHRRINSKKKE-----SAWEMTKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWM 126
                                                                                                                                                                                                                                                                                                                             240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDVY----GNKQFTVLTAYGLQVRDINELVTKMNVTGFPVVESLSDVTLLGYAPVKKIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADVMRPRRNDPPLAVLTQDNMTVDDIENMINETSYNGFPVIMSKESQRLVGFALRRDLTI 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSLV
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                                                                                 ---KFSLNYLIYTAFALLFVLCAAIMVRDVAPLAAGSGISEIKCIISGFLRDSFLSFRVM
                                                                                                                                                                 SDIRRGYCTSHWYYNEKFCCWYSETMGMFKHDLYNDLTF-QGSSCTAWKPWTY------
                                                                                                                                                                                                                                              KDRV-NEIINEQNEENVIDQSRWSKLWRIWNVGYSWFILSIIGTTVGFAAYMLDIVTSWL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFRKLGLRQCLVTHNGRLLGIITKKDILRHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIESARKKQEGIVGSSRVCFAQHTPSLPAESP-RPLKLRSILDMSPFTVTDHTPMEIVVD
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                                                                                                                                                                                                                                                                                                                             Conservative 142;
                                                                                                                                                                                                                                                                                                                           24.3%; Score 1015; DB 2; 32.0%; Pred. No. 1.6e-71; ative 142; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrell, B.G.; Lucas, M.; Gaillardin,
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                              VVDIFRKLGLRQCLVTHNGRLLGIITKKDIL 774
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VAVLFEVLSPSVIFIEKDGNLVGLISKKDLL 768
                                                                                                                                                                             DPPLAYLTQDNMTVDDIE------NMINETSYNGFPVIMSKESQRLVGFALRRDLTIAI
                                                                                                                                                                                                                                       LEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTLAADVMRPRRN
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                                                                      EAA-KLEPSFTFDQQLCFGKVDSVGDSKSSKFGESDR-IDLSAYMDVNPISVLHTQSIAN
                                                                                                                                           IPITEVMASNLITIPSIGFTWRKLLGMMEGYDFSGYPVVLDSRSNYLIGYLKKSSLKSSF
                                                                                                                                                                                                                  LNFILPTVLVVALANSIGNMLGKTGIADRSIEINGLPLLEPEKSINSSNTI-----N
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                                                                                                       ESARKKQEGIVGSSRVCFAQ-----HTPSLPAESPRPLKLRSILDMSPFTVTDHTPMEI
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chloride channel protein CLC-1 - yeast (Saccharomyces cerevisiae) W;Alternate names: protein GTC779; protein J1616; protein YJR040w C;Species: Saccharomyces cerevisiae C;Pate: 13-dan-1995 #sequence_revision 24-Feb-1995 #text_change 2 C;Accession: S50054; S39904; S57059; S63763
A;Cross-references: EMBL:249540; NID:g1015690; R;Huang, M.E.; Chuat, J.C.; Galibert, F. Yeast 11, 775-781, 1995
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-12,'R',14-206,'L',208-256,'T',258-261,'L',263-496,'I',498-779
A; Cross references: EMBL: Z23117; NID: g619512; PIDN: CAA80663.1; PID: g435539
R; Huang, M.E.; Chuat, J.C.; Gallbert, F.
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:L29347; NID:g576927; PIDN:AAA53399.1; PID:g576928 R;Greene, J.R.; Brown, N.H.; DiDomenico, B.J.; Kaplan, J.; Eide, D.J. Mol. Gen. Genet. 241, 542-553, 1993 Mol. Gen. Genet. 241, 542-553, 1993 A;Title: The GEF1 gene of Saccharomyces cerevisiae encodes an integral meml A;Reference number: S39904; MUID:94088447; PMID:7505388 A;Accession: S39904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Huang, M.E.; Chuat, J.C.; Galibert, F.
J. Mol. Biol. 242, 595-598, 1994
A; Tritle: A voltage-gated chloride channel in the yeast SA; Reference number: S50054; MUID:95018225; PMID:7932715
A; Accession: S50054
A; Status: nucleic acid sequence not shown
                                                                                                       A; Molecule type: DNA
A; Residues: 1-779 < MAN>
                                                                                                                                                                             A; Reference number: S57052
A; Accession: S57059
                                                                                                                                                                                                                                                   submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-779 <HUA>
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                                                                         PIDN:CAA89567.1;
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                                                                      PID:g1015691;
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A;Title: An:
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A;Reference

number:

S63757;

kb DNA sequence MUID:95397595; I

of chromosome PMID:7668047

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three

tRNA genes

Analysis of a 42.5

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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-779 <HUW>
A;Cross-references: EMBL:L36344; NID:g1197060; PIDN:AAA88741.1; PID:g1197067
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 19
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                                                                                                                                                                                                                                                                                                            TRMTVSLVVIVFELTGGLEYIVPLMAAVMTSKWVGDAFG-REGIYEAHIRLNGYPFL---
                                                                                                                                                                                                                                                                                                                                                                                  ----LCDYRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFFAALVAAFVLRSINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRAN 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KE----SQRLVGFALRRDLT--IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIPSMAIGAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCCWG-----SNETTF 154
EDKFEKEKRCIGYVLKRHLASKIMMQSVNSTK - - - AQTTLVYFNKSNEEL - GHRENCIGF 684
                                                                                                                                 QDEEEEETLEKYTAEQLMSSK-----LITINETIYLSELESLLYDSASEYSVHGFPITKD
                                                                                                                                                                                            -DAKEEFTHTTLAADVMRPRRNDPPLAVLTQDNMTVDDIENMI----NETSYNGFPVIMS
                                                                                                                                                                                                                                                                  TNLTLTVVVVIMFELTGAFMYIIPLMIVVAITRIILSTSGISGGIADQMIMVNGFPYLEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQEFECEAQGLWIAWK-------GHVSPFIIFMLLSVLFALISTLLVKYVAPMATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPETQNFDQFVTIDKIAEENRPLSVDSDRE---FLNSKYRHYREVIWDRAKT-----F 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPGVGTYDDFHTIDWVREKCK-----DRERHRRINSK---KKESAWEMTKSLYDAWSGW 102
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Qy 560 TRMTVSLVVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKE 619	Qy 500 FIPSMAIGAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGV 559 : : : Db 512 FIPAILTGAAWGRLFGIFVERLFPSVTGIDPGKYALAGAAAQLGGV 557	Qy 443 SLCDYRNDMNASKIVDDIPDRPAGTGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGL 499 : :: :	Qy 396 FGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESS 442 :	Qy 347LVLEYVEYHTDWYLFELFPFILLGVFGGLWGAFFIRANIAWCRRRKSTK 395	Qy 287 LSAASAAGVSVAFGAPIGGVLFSLBEVSYYFPLKTLWRSFFAALVAAFVLRSINPFGNSR 346 : : : : :::: : : : : : :	Qy 238 KTITLVLAVASGLSLGKEGPLVHVACCCGNIFSYLFPKYSTNEAKKREV 286	Qy 178 GSYIMNYIMYIFWALSFAFLAVSLVKVFAPYACGSGIPEIKTILSGETIRGYLGKWTLMI 237 : : :	QY 118 LIDIAADWMTDLKBGICLSALWYNHEQCCWGSNETTFEERDKCPQWKTWAELIIGQABGP 177	Qy 75 -ERHRRINSKKKESAWEMTKS-LY-DA	Qy 30 YTMTNGGSINSSTHLLDLLDEPIPGVGTYDDFHTIDWVREKCKDR 74 : : : : : :: : : : :: : :: : :: : ::	Query Match 18.5%; Score 773; DB 2; Length 810; Best Local Similarity 28.8%; Pred. No. 1.7e-52; Matches 247; Conservative 141; Mismatches 296; Indels 174; Gaps 28;	A; Residues: 1-810 < WIL> A; Cross-references: EMBL: 275955; PIDN: CAB00111.1; GSPDB: GN00023; CESP: R07B7.1 A; Cross-references: clone R07B7 C; Genetics: A; Gene: CESP: R07B7.1 A; Map position: 5 A; Introns: 27/2; 57/3; 106/3; 153/1; 217/3; 481/1; 626/2; 717/2; 778/3	Harris, bmitted Referen Accessi Status:	RESULT 12 T24009 Typothetical protein R07B7.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-oct-1999 C;Accession: T24009	QY 725 RSILDMSPETVTDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKKDILR 775 : ::

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R;Brandt, S.; Jentscn, 1...
R;Brandt, S.; Jentscn, 1995
FEBS Lett. 377, 15-20, 1995
A;Title: CLC-6 and CLC-7 are two novel broad-formation of the companies of 
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F; 407-432/Domain:
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C; Keywords: ion
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A;Residues: 1-414,'A',415-528,'M',530-802 <BRW>
A;Cross-references: EMBL:267744; NID:91177612; PIDN:CAA91557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A; Description: CLC-6 and CLC-7 are
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A;Residues: 1-802 <BRA>
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325-343/Domain:
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              156
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                                                                                                                                           DRERHRRINSKKKESAWEMTKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEG 132
              Y
                                                                                                FLEEERRIN----HTAFRTVEI-----KRWVICALIGILTGLVACFIDIVVENLAGLKYR 155
                                                   ICLSALWYNHEQCCWGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWA- 191
                                                                                                                                                                                                                                     RGTHYTMTNGGSINSSTHLLDLLDEPIPGVGTYD------DFHTIDWVR-EKCK 72
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                                                                                                                                                                                                                                                                                      11 Similarity
248; Conser
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Pred. No. 8.
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two novel
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on 13-Mar-1997 #text_change 20-Jun-2000
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A; Residues: 1-789 < BRA>
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                                                                                                                                                                                        A; Cross-references: EMBL: 267743;
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  Best Local Sin
Matches 239;
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    Similarity 30.1
39; Conservative
                                                                                              16p13-16p13
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                                                                                                                      GDB:3929156
18.0%; Sco
30.1%; Pro
ative 126;
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R:Brandt, S.; Jentsch, T.J.
FEBS Lett. 377, 15-20, 1995
A;Title: CLC-6 and CLC-7 are two novel broadly expressed
A;Reference number: S68426; MUID:96130311; PMID:8543009
A;Accession: S68427
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chloride channel protein 7 (C1C-7) - human
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                                                                                                                                                                                                           NID: g1177439;
                       Score 750.5;
Pred. No. 9.
                                                                                                                                                                                                                                                                                  sequence not shown
  Mismatches
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                       9.7e-51;
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                                                                                                                                                                                                           PIDN:CAA91556.1;
                                                  DB 2;
     243;
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                                                                                                                                                                                                                                                                                                                                                            CLC chloride
  36;
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probable chloride channel CIC-6 - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S68428; S51659
R;Brandt, S; Jentsch, T J
FEBS Lett. 377, 15-20, 1995
A;Title: CIC-6 and CIC-7 are two novel broadly expressed members
                                                                         A; Reference number: A; Accession: S68428
                   A; Molecule type: mRNA
A; Residues: 1-869 < BRA>
                                                       A; Status: nucleic acid sequence
   A; Cross-references:
                                                                                                                                                                                                                                                             RESULT 15
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 NID: g1154676;
                                                                                          novel broadly expressed:96130311; PMID:8543009
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 PIDN:CAA58292.1;
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C;Keywords: chloride channel; glycoprotein; transmembrar

F;81-98/Domain: transmembrane #status predicted <TM1>

F;126-156/Domain: transmembrane #status predicted <TM2>

F;179-198/Domain: transmembrane #status predicted <TM3>
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F;371-396/Domain:
F;462-507/Domain:
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                                                                                                                                                                                RPRRNDPPLAYLTQDNMT------VDDIENMINETSYNGFPVI--------
                                                                                                                                                                                                                       STNEITYGLPIMVTLMVAKWTGDFFNK-GIYDIHVGLRGVPLLEWETEVEMDKLRASDIM
                                                                                                                                                                                                                                              LTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL-AADVM
                                                                                                                                                                                                                                                                                              LVANVLKSY-------IGLGHIYSGTFALIGAAAFLGGVVRMTISLTVILIE
                                                                                                                                                                                                                                                                                                                                                                                                             --PDRPAGI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt KCYLNGVKVPGIVRLRTLLCKVLGVLFSVAGGLFVGKEGPMIHSGSVVGAGLPQFQSISL}
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RYTPYPNLYPDQSPSEDWTMEERFRPLTFHGLILRSQLVTLLVRGVCYSESQSS--ASQP
                                                                         ISNNIKFKKSSILTRAGEQRKRSQSMKSYPSSELRNMCDEHIASEEPAEKEDLLQQMLER
                                                                                                                                                  EP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VASMVLGECRQMSSSS--QIGNDSFQLQVTEDVNSSIKTFFCPNDTYNDMATLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIGGLLGATEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCSMSATFTLNFFRSGIQFGSWGSFQLPGLLNFGEFKCSDSDKKCHLWTAMDLGFFVVMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --CSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane #status predicted transmembrane #status predicted transmembrane #status predicted transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status predicted <TM9>
transmembrane #status predicted <TM11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SINPEGNSRL--VLFYVEYHTP-----WYLFELFPFILLG
                                                                                                                                                                                                                                                                                                                                                                                                         -GVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAIGAIAGR
                                                                                                                                                -NLTYVYPHTRIQSLVSILRTTVHHAFPVVTENRGNEKEFMKGNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CLNKRLAKYRMRNVHPKPKLVRVLESLLVSLVTTVVVF-----
                                                                                                           --MSKESQRLVGF---ALRR--DLTIAIESARKKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KGCLALSLLELLGFNLTFVFLA-SLLVLIEDVAAGSGIPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1e-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 725.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                    -GIVGSSR------VCFAQHTPSLPAESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <8MT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QTSVEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    719
                                                                         712
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460

421

370 281

341

390

222

266

80

35

Qy

Ъ Qy Db

QΥ В

В

697 652 668 605 631 546 572 501 512 QY

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В Qy 밁 ρy Qy DЪ δÃ

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